

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Bandman, Olga
Hillman, Jennifer L.
Lal, Preeti
Corley, Neil C.
Shah, Purvi
- (ii) TITLE OF THE INVENTION: HUMAN RETICULOCALBIN ISOFORMS
- (iii) NUMBER OF SEQUENCES: 6
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
(B) STREET: 3174 Porter Drive
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Hereewith
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Billings, Lucy J.
(B) REGISTRATION NUMBER: 36,749
(C) REFERENCE/DOCKET NUMBER: PF-0358 US
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 650-855-0555
(B) TELEFAX: 650-845-4166
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 328 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
(A) LIBRARY: RATRNOT02
(B) CLONE: 922578

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Met | Trp | Arg | Pro | Ser | Val | Leu | Leu | Leu | Leu | Leu | Leu | Arg | His |
| 1 | | | | 5 | | | | 10 | | | | | 15 | |
| Gly | Ala | Gln | Gly | Lys | Pro | Ser | Pro | Asp | Ala | Gly | Pro | His | Gly | Gln |
| | | 20 | | | | | | 25 | | | | | 30 | |
| Arg | Val | His | Gln | Ala | Ala | Pro | Leu | Ser | Asp | Ala | Pro | His | Asp | Ala |
| | | 35 | | | | | 40 | | | | | 45 | | |
| His | Gly | Asn | Phe | Gln | Tyr | Asp | His | Glu | Ala | Phe | Leu | Gly | Arg | Glu |
| | | 50 | | | | 55 | | | | 60 | | | | Val |
| Ala | Lys | Glu | Phe | Asp | Gln | Leu | Thr | Pro | Glu | Glu | Ser | Gln | Ala | Arg |
| | | 65 | | | 70 | | | | 75 | | | | | 80 |
| Gly | Arg | Ile | Val | Asp | Arg | Met | Asp | Arg | Ala | Gly | Asp | Gly | Asp | Gly |
| | | | | 85 | | | | | 90 | | | | | 95 |
| Val | Ser | Leu | Ala | Glu | Leu | Arg | Ala | Trp | Ile | Ala | His | Thr | Gln | Gln |
| | | | | 100 | | | | 105 | | | | | 110 | |
| His | Ile | Arg | Asp | Ser | Val | Ser | Ala | Ala | Trp | Asp | Thr | Tyr | Asp | Thr |
| | | 115 | | | | | 120 | | | | | 125 | | |
| Arg | Asp | Gly | Arg | Val | Gly | Trp | Glu | Glu | Leu | Arg | Asn | Ala | Thr | Tyr |
| | | 130 | | | | 135 | | | | | 140 | | | Gly |
| His | Tyr | Ala | Pro | Gly | Glu | Glu | Phe | His | Asp | Val | Glu | Asp | Ala | Glu |
| | | 145 | | | 150 | | | | 155 | | | | | Thr |
| Tyr | Lys | Lys | Met | Leu | Ala | Arg | Asp | Glu | Arg | Arg | Phe | Arg | Val | Ala |
| | | | 165 | | | | | 170 | | | | | | 175 |
| Gln | Asp | Gly | Asp | Ser | Met | Ala | Thr | Arg | Glu | Glu | Leu | Thr | Ala | Phe |
| | | | 180 | | | | 185 | | | | | 190 | | Leu |
| His | Pro | Glu | Glu | Phe | Pro | His | Met | Arg | Asp | Ile | Val | Ile | Ala | Glu |
| | | 195 | | | | | 200 | | | | | 205 | | Thr |
| Leu | Glu | Asp | Leu | Asp | Arg | Asn | Lys | Asp | Gly | Tyr | Val | Gln | Val | Glu |
| | | 210 | | | | 215 | | | | 220 | | | | Glu |
| Tyr | Ile | Ala | Asp | Leu | Tyr | Ser | Ala | Glu | Pro | Gly | Glu | Glu | Pro | Ala |
| | | 225 | | | 230 | | | | 235 | | | | | 240 |
| Trp | Val | Gln | Thr | Glu | Arg | Gln | Gln | Phe | Arg | Asp | Phe | Arg | Asp | Leu |
| | | | 245 | | | | | 250 | | | | | | 255 |
| Lys | Asp | Gly | His | Leu | Asp | Gly | Ser | Glu | Val | Gly | His | Trp | Val | Leu |
| | | | 260 | | | | 265 | | | | | 270 | | Pro |
| Pro | Ala | Gln | Asp | Gln | Pro | Leu | Val | Glu | Ala | Asn | His | Leu | Leu | His |
| | | 275 | | | | 280 | | | | | | 285 | | Glu |
| Ser | Asp | Thr | Asp | Lys | Asp | Gly | Arg | Leu | Ser | Lys | Ala | Glu | Ile | Leu |
| | | 290 | | | 295 | | | | | 300 | | | | Gly |
| Asn | Trp | Asn | Met | Phe | Val | Gly | Ser | Gln | Ala | Thr | Asn | Tyr | Gly | Glu |
| | | 305 | | | 310 | | | | 315 | | | | | 320 |
| Leu | Thr | Arg | His | His | Asp | Glu | Leu | | | | | | | |
| | | | | | | 325 | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: RATRNOT02
- (B) CLONE: 922578

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CGCAGAGCGG | ACGTGGAGAG | CGGACGNCAG | CTGGATAACA | GGGGACCGAT | GATGTGGCGA | 60 |
| CCATCAGTTC | TGCTGCTTCT | GTTGCTACTG | AGGCACGGGG | CCGAGGGGAA | GCCATCCCCA | 120 |

| | | | | | | |
|------------|------------|-------------|------------|------------|-------------|------|
| GACGCAGGCC | CTCATGGCCA | GGGGAGGGTG | CACCAGGCGG | CCCCCTGAG | CGACGCTCCC | 180 |
| CATGATGACG | CCCACGGGAA | CTTCCAGTAC | GACCATGAGG | CTTTCTCTGG | ACGGGAAGTG | 240 |
| GCCAAGGAAT | TCGACCAACT | CACCCCAGAG | GAAGGCCAGG | CCCGTCTGGG | GCGGATCGTG | 300 |
| GACCGCATGG | ACCGCCGGGG | GGACGGCGAC | GGCTGGGTGT | CGCTGGCCGA | GCTTCGCGCG | 360 |
| TGGATCGCGC | ACACGCAGCA | GCGGCACATA | CGGGACTCGG | TGAGCGCGCG | CTGGGACACG | 420 |
| TACGACACGG | ACCGCGACGG | GCGTGTGGGT | TGGGAGGAGC | TGCGCAACGC | CACCTATGCG | 480 |
| CACCTACCGC | CCGGTGAAGA | ATTTCATGAC | GTGGAGGATG | CAGAGACCTA | CAAAAAGATG | 540 |
| CTGGCTCGGG | ACAGGCGGCG | TTTCCGGGTG | GCGCAGCAGG | ATGGGGACTC | GATGGCCATG | 600 |
| CGAGAGGAGC | TGACAGCCTT | CCTGCACCCC | GAGGAGTTCC | CTCACATGCG | GGACATCTGT | 660 |
| ATTCTGAAAA | CCCTGGAGGA | CCTGGACAGA | AACAAAGATG | GCTATGTCCA | GGTGGAGGAG | 720 |
| TACATCGCGC | ATCTGTACTC | AGCCGAGCCT | GCGGAGGAGG | AGCCGCGCTG | GSTGCAGACG | 780 |
| GAGAGCGAGC | AGTTCCGGGA | CTTCCGGGAT | CTGACACAGG | ATGGGCACCT | GGATGGGACT | 840 |
| GAGGTGGGCG | ACTGGGTGCT | GCCCCCTGCC | CAGGACACGC | CCCTGGTGGA | AGCCCAACCAC | 900 |
| CTGTCTGACG | AGAGCGAGAC | GGACAAGGAT | GGCGGGCTGA | GCAAAAGCGA | AATCTGGGTG | 960 |
| AATTGGAACA | TGTTTGTGGG | CAGTCAGGCC | ACCAACTATG | GCGAGGACCT | GACCCGGCAC | 1020 |
| CACGATGAGC | TGTTGAGCAC | GCGCACCTGC | CACAGCCTCA | GAGGCCCGCA | CAATGACCGG | 1080 |
| AGGAGGGGCC | GCTGTGGTCT | GCCCCCTTCC | CTGTCCAGGC | CCCGCAGGAG | GCAGATGACG | 1140 |
| TCCAGGGCAT | CTTCCCTGCC | CTGGGCTCTC | AGGGACCCCC | TGGGTGCGGT | TCTGTCCCTG | 1200 |
| TCACACCCCC | AACCCGAGGG | AGGGGCTGTC | ATAGTCCGAG | AGGATAAGCA | ATACCTATTG | 1260 |
| CTGACTGAGT | CTCCGAGCCC | AGACCCAGGG | ACCCTTGGCC | CCAAGCTCAG | CTCTAAGAAC | 1320 |
| CGCCCCAACC | CTCTCAGCTC | CAAACTCTGAG | CCTCCACCAC | ATAGACTGAA | ACTCCCCTGG | 1380 |
| CCCCAGCCCT | CTCTGCGCTG | GCTTGGCCTG | GGACACCTCC | TCTCTGCCAG | GAGGCAATAA | 1440 |
| AAGCCAGCGC | CGGGAAGAAA | AAA | | | | 1463 |

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BLADNOT03
 (B) CLONE: 1601793

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Asp | Leu | Arg | Gln | Phe | Leu | Met | Cys | Leu | Ser | Leu | Cys | Thr | Ala | Phe |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Ala | Leu | Ser | Lys | Pro | Thr | Glu | Lys | Lys | Asp | Arg | Val | His | His | Glu | Pro |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Gln | Leu | Ser | Asp | Lys | Val | His | Asn | Asp | Ala | Gln | Ser | Phe | Asp | Tyr | Asp |
| | | | 35 | | | | 40 | | | | | 45 | | | |
| His | Asp | Ala | Phe | Leu | Gly | Ala | Glu | Ala | Lys | Thr | Phe | Asp | Gln | Leu | |
| | | | 50 | | | 55 | | | | 60 | | | | | |
| Thr | Pro | Glu | Glu | Ser | Lys | Glu | Arg | Leu | Gly | Lys | Ile | Val | Ser | Lys | Ile |
| | | | 65 | | 70 | | | | 75 | | | | 80 | | |
| Asp | Gly | Asp | Lys | Asp | Gly | Phe | Val | Thr | Val | Asp | Glu | Leu | Lys | Asp | Trp |
| | | | 85 | | | | | 90 | | | | | 95 | | |
| Ile | Lys | Phe | Ala | Gln | Lys | Arg | Trp | Ile | Tyr | Glu | Asp | Val | Glu | Arg | Gln |
| | | | 100 | | | | 105 | | | | | 110 | | | |
| Trp | Lys | Gly | His | Asp | Leu | Asn | Glu | Asp | Gly | Leu | Val | Ser | Trp | Glu | Glu |
| | | | 115 | | | 120 | | | | | | 125 | | | |
| Tyr | Lys | Asn | Ala | Thr | Tyr | Gly | Tyr | Val | Leu | Asp | Asp | Pro | Asp | Pro | Asp |
| | | | 130 | | | 135 | | | | | 140 | | | | |
| Asp | Gly | Phe | Asn | Tyr | Lys | Gln | Met | Met | Val | Arg | Asp | Glu | Arg | Arg | Phe |
| | | | 145 | | 150 | | | | | 155 | | | | 160 | |
| Lys | Met | Ala | Asp | Lys | Asp | Gly | Asp | Leu | Ile | Ala | Thr | Lys | Glu | Glu | Phe |
| | | | 165 | | | | 170 | | | | | | | 175 | |

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Thr Ala Phe Leu His Pro Glu Glu Tyr Asp Tyr Met Lys Asp Ile Val
      180      185      190
Val Gln Glu Thr Met Glu Asp Ile Asp Lys Asn Ala Asp Gly Phe Ile
      195      200      205
Asp Leu Glu Glu Tyr Ile Gly Asp Met Tyr Ser His Asp Gly Asn Thr
      210      215      220
Asp Glu Pro Glu Trp Val Lys Thr Glu Arg Glu Gln Phe Val Glu Phe
      225      230      235
Arg Asp Lys Asn Arg Asp Gly Lys Met Asp Lys Glu Thr Lys Asp
      245      250      255
Trp Ile Leu Pro Ser Asp Tyr Asp His Ala Glu Ala Glu Ala Arg His
      260      265      270
Leu Val Tyr Glu Ser Asp Gln Asn Lys Asp Gly Lys Leu Thr Lys Glu
      275      280      285
Glu Ile Val Asp Lys Tyr Asp Leu Phe Val Gly Ser Gln Ala Thr Asp
      290      295      300
Phe Gly Glu Ala Leu Val Arg His Asp Glu Phe
      305      310      315

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2658 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BLADNOT03
 (B) CLONE: 1601793

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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CCCCGCTCCG GTTGGGCGGT GCTTGCAGCG GTGAGCTGAG CCGGTGGGGT AGCGGCGGCC 60
ACGGCATCCT GTGCTGTGGG GGCTACGAGG AAAGATCTAA TTATCATGGA CCTGCGACAG 120
TTTCTTATGT GCCTGTCCCT GTGCACAGCC TTTCCTTTGA GCAAACCCAC AGAAAAGAG 180
GACCGTGATC ATCATGAGCC TCAGCTCAGT GACAAGGTTC ACAATGATGC TCAGAGTTT 240
GATTATGACC ATGATGCTTT CTTGGGTGCT GAAGAAGCAA AGACCTTTGA TCAGCTGACA 300
CCAGAAGAGA GCAAGAAAGG GCTTGGAAAG ATTGTAAGTA AATAGATGG CGACAAGGAC 360
GGGTTTGCTA CTTGTGATGA GCTCAAAGAC TGGATTAAT TTGCACAAAA CGCTGGATT 420
TACGAGGATG TAGAGCGACA GTGGAAGGGG CATGACCTCA ATGAGGACGG CCTCGTTTCC 480
TGGGAGGAGT ATAAAAATGC CACCTACGGC TACGTTTTAG ATGATCCAGA TCCTGATGAT 540
GGATTTAACT ATAAACAGAT GATGGTTAGA GATGAGCGGA GGTTTAAATAT GGCAGACAAG 600
GATGGAGACC TCATTGCCAC CAAGGAGGAG TTCACAGCTT TCCTGCACCC TGAGGAGTAT 660
GACTACATGA AAGATATAGT AGTACAGGAA ACAATGGAAG ATATAGATAA GAATGCTGAT 720
GGTTTCACTG ATCTAGAAGA GTATATTGGT GACATGTACA GCATGATGAG GAATACTGAT 780
GAGCCAGAAT GGGTTAAGAC AGAGCGAGAG CAGTTTGTGT AGTTTCGGGA TAAGAACCCT 840
GATGGGAAGA TGGCAAGAGA AGAGACAAAA GACTGGATCC TTCCCTCAGA CTATGATCAT 900
GCAGAGCGCA AGATCAGGCA CCTGGTCTAT GAATCAGACC AAAACAAGGA TGGCAAGCTT 960
ACCAGAGGAG AGATCGTTGA CAAGTATGAC TTATTTGTGT GCAGCGACCG CACAGATTTT 1020
GGGAGGSCCT TAGTACGCTC TGATGAGTTC TGAGCTACGG AGGAACCCCT ATTTCCCTAA 1080
AAGTAATTTA TTTTACAGC TTCTGGTTTC ACATGAAATT GTTTCGCCTA CTGAGACTGT 1140
TACTACAAAC TTTTAAAGC ATGAAAAGGC GTAATGAAAA CCATCCCGCT CCCATTCCCT 1200
CTCCTCTCTG AGGGACTGGA GGGGAAGCGT GCTTCTGAGG AACAACTCTA ATTAGTACAC 1260
TTGTGTTTGT AGATTACAC TTTGTATTAT GTATTAACAT GCGGTGTTTA TTTTGTATT 1320
TTTCTCTGCT TGGGAGTATT ATATGAAGGA TCAAGATCCT CAACTCACAC ATGTAGACAA 1380
ACATTAGCTC TTACTCTTT TCAACCCCT TTTATGATT TTAATAATCT CACTTAACTA 1440
ATTTTGTAAG CCTGAGATCA ATAAGAAATG TTCAGGAGAG AGGAAAGAAA AAAAATATAT 1500
GTTCCCAAT TTATATTAG AGAGAGAACA CTTAGTCTTG CTGTCAAAA AGTCCAACAT 1560
TTCATAGGTA GTAGGGGCCA CATATTACAT TCAGTTGCTA TAGGTCCAGC AACTGAACCT 1620
GCCATTACCT GGGCAAGGAA AGATCCCTTT GCTCTAGGAA AGCTTGGCCC AAATTGATT 1680

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TCTTCTTTT CCCCCGTAG GACTGACTGT TGGCTAATTT TGTCAAGCAC AGCTGTGGTG 1740
GGAAGAGTTA GGGCCAGTGT CTTGAAAATC AATCAAGTAG TGAATGTGAT CTCTTTGCGAG 1800
AGCTATAGAT AGAAACAGCT GGAACACTAA AGGAAAAATA CAAATGTTTT CGGGGCATAC 1860
ATTTTTTTTC TGGGTGTGCA TCTGTGTGAA TGCTCAAGAC TTAATTTATT GCCTTTTGAA 1920
ATCACTGTAA ATGCCCCCAT CCGGTTCCCTC TTCTTCCAG GTGTGCCAAG GAATTAATCT 1980
TGGTTTCACT ACAATTAAAA TTCACTTCCTT TCCAATCATG TCATTTGAAAG TGCCTTTAAC 2040
GAAAGAAATG GTCACTGAAT GGGAAATTCTC TTAAGAAACC CTGAGATTAA AAAAAGACTA 2100
TTTGGATAAC TTATAGGAAA GCCTAGAAC TCCCAGTAGA GTGGGGATTT TTTTCTCTTT 2160
CCCTTCTCTT TTTGGACAAT AGTTAAATTA GCAGTATTAG TTATGAGTTT GGTGCGAGTG 2220
TTCTTATCTT GTGGGCTGAT TTCCAAAAC CACATGCTGC TGAATTTACC AGGGATCCCT 2280
ATACCTCACA ATGCAAAACA CTTACTACCA GGCCTTTTTC TGTGTCCACT GGAGAGCTTG 2340
AGCTCACACT CAAGATCAG AGGACCTACA GAGAGGGCTC TTTGTTTGA GCACCATGGC 2400
TTACCTTTCC TGCTTTTGAC CCATCACACC CCATTTCCCTC CTCTTTCCCT CTCGCCGCTG 2460
CCAAAAAATA AAAAAAGGA AACGTTTATC ATGAATCAAC AGGGTTTCAG TCCTTATCAA 2520
AGAGAGATGT GAAAGAGCT AAAGAAACCA CCCTTTGTTT CCAACTCCAC TTACCCATA 2580
TTTTATGCAA CACAAACACT GTCCTTTTGG GTCCCTTCTT TACAGATGGG ACCTCTTGAG 2640
GAAGGAATTA TCGTATTC 2658

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(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1262329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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Met Ala Arg Gly Gly Arg Gly Arg Arg Leu Gly Leu Ala Leu Gly Leu
 1           5           10           15
Leu Leu Ala Leu Val Leu Ala Pro Arg Val Leu Arg Ala Lys Pro Thr
 20          25          30
Val Arg Lys Glu Arg Val Val Arg Pro Asp Ser Glu Leu Gly Glu Arg
 35          40          45
Pro Pro Glu Asp Asn Gln Ser Phe Gln Tyr Asp His Glu Ala Phe Leu
 50          55          60
Gly Lys Glu Asp Ser Lys Thr Phe Asp Gln Leu Thr Pro Asp Glu Ser
 65          70          75
Lys Glu Arg Leu Gly Lys Ile Val Asp Arg Ile Asp Asn Asp Gly Asp
 85          90          95
Gly Phe Val Thr Thr Glu Glu Leu Lys Thr Trp Ile Lys Arg Val Gln
100          105          110
Lys Arg Tyr Ile Phe Asp Asn Val Ala Lys Val Trp Lys Asp Tyr Asp
115          120          125
Arg Asp Lys Asp Asp Lys Ile Ser Trp Glu Glu Tyr Lys Gln Ala Thr
130          135          140
Tyr Gly Tyr Tyr Leu Gly Asn Pro Ala Glu Phe His Asp Ser Ser Asp
145          150          155
His His Thr Phe Lys Lys Met Leu Pro Arg Asp Glu Arg Arg Phe Lys
165          170          175
Ala Ala Asp Leu Asn Gly Asp Leu Thr Ala Thr Arg Glu Glu Phe Thr
180          185          190
Ala Phe Leu His Pro Glu Glu Phe Glu His Met Lys Glu Ile Val Val
195          200          205
Leu Glu Thr Leu Glu Asp Ile Asp Lys Asn Gly Asp Gly Phe Val Asp
210          215          220

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| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Gln | Asp | Glu | Tyr | Ile | Ala | Asp | Met | Phe | Ser | His | Glu | Glu | Asn | Gly | Pro | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | |
| Glu | Pro | Asp | Trp | Val | Leu | Ser | Glu | Arg | Glu | Gln | Phe | Asn | Glu | Phe | Arg | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| Asp | Leu | Asn | Lys | Asp | Gly | Lys | Leu | Asp | Lys | Asp | Glu | Ile | Arg | His | Trp | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| Ile | Leu | Pro | Gln | Asp | Tyr | Asp | His | Ala | Gln | Ala | Glu | Ala | Arg | His | Leu | |
| | | | 275 | | | | 280 | | | | | 285 | | | | |
| Val | Tyr | Glu | Ser | Asp | Lys | Asn | Lys | Asp | Glu | Lys | Leu | Thr | Lys | Glu | Glu | |
| | | | 290 | | | 295 | | | | | 300 | | | | | |
| Ile | Leu | Glu | Asn | Trp | Asn | Met | Phe | Val | Gly | Ser | Gln | Ala | Thr | Asn | Tyr | |
| 305 | | | | 310 | | | | | 315 | | | | | | 320 | |
| Gly | Glu | Asp | Leu | Thr | Lys | Asn | His | Asp | Glu | Leu | | | | | | |
| | | | 325 | | | | | 330 | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 780361

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Arg | Arg | Asp | Val | Ala | Lys | Glu | Phe | Asp | Gln | Leu | Thr | Pro | Glu | Glu | Ser | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | |
| Gln | Ala | Arg | Leu | Gly | Arg | Ile | Val | Asp | Arg | Met | Asp | Leu | Ala | Gly | Asp | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Ser | Asp | Gly | Trp | Val | Ser | Leu | Ala | Ala | Leu | Arg | Ala | Trp | Ile | Ala | His | |
| | | | 35 | | | 40 | | | | | | 45 | | | | |
| Thr | Gln | Gln | Arg | His | Ile | Arg | Asp | Ser | Val | Ser | Ala | Ala | Trp | His | Thr | |
| | | | 50 | | | 55 | | | | 60 | | | | | | |
| Tyr | Asp | Thr | Asp | Arg | Asp | Gly | Arg | Val | Gly | Trp | Glu | Glu | Leu | Arg | Asn | |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | | |
| Ala | Thr | Tyr | Gly | His | Tyr | Glu | Pro | Gly | Glu | Glu | Phe | His | Asp | Val | Glu | |
| | | | | 85 | | | | 90 | | | | | | 95 | | |
| Gly | Pro | | | | | | | | | | | | | | | |

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☐ Page(s) _____ of _____ were not present
for scanning. (Document title)

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